AMENDMENTS TO THE CLAIMS

Claim 1 (Currently Amended): A method for producing a protein having an antithrombotic activity, which comprises replacing, in a protein that has an amino acid sequence ~~having a sequence identity of not less than 30% to the amino acid sequence~~ of SEQ ID NO: 1 and forms a tertiary structure, from N-terminus to C-terminus, composed of a first β strand (β1), a first a helix (αl), a second α helix (α2), a second β strand (β2), a loop, a third β strand (β3), a fourth β strand (β4) and a fifth β strand (β5) in this order from the amino terminus, at least one amino acid residue in a region from α2 to β2, a region from β3 to β4, or in the regions from α2 to β2 and from β3 to β4 so that electric charge of the amino acid residue is substituted towards positive direction as compared to the unsubstituted amino acid.

Claim 2 (Previously Presented): The method according to Claim 1, wherein at least one acidic amino acid residue in the region from α2 to β2, a region from β3 to β4, or in the regions from α2 to β2 and from β3 to β4 is replaced with a neutral amino acid residue to change electric charge of the amino acid residue towards positive direction as compared to the unsubstituted amino acid.

Claim 3 (Previously Presented): The method according to Claim 1, wherein the protein originates from *Crotalus horridus horridus*.

Claim 4 (Previously Presented): The method according to Claim 1, wherein the region from α2 to β2 in the protein corresponds to the sequence of the amino acid residues 47 to 72 in the amino acid sequence of SEQ ID NO: 1 and the region from β3 to β4 corresponds

to the sequence of the amino acid residues 94 to 111 in the amino acid sequence of SEQ ID NO: 1.

Claim 5 (Previously Presented): The method according to Claim 4, wherein at least one acidic amino acid residue of which α carbon atom exists within 10 Å from the α carbon atom of the arginine residue of the amino acid residue 103 in the amino acid sequence of SEQ ID NO: 1 is replaced with a neutral amino acid residue.

Claim 6 (Previously Presented): The method according to Claim 5, wherein the acidic amino acid residue is at least one residue selected from the aspartic acid residue of the amino acid residue 54, the aspartic acid residue of the amino acid residue 101 and the glutamic acid residue of the amino acid residue 106 in the amino acid sequence of SEQ ID NO: 1.

Claim 7 (Currently Amended): The method according to Claim 1, which further comprises deleting a region containing the loop structure existing between β2 and β3 in such a manner that the secondary or tertiary structures of β2 and β3 are maintained, or replacing the region with one or more amino acid residue(s) in a number required to maintain the secondary ~~or~~ and tertiary structures of β2 and β3, said amino acid residue(s) being selected from the group consisting of a glycine residue, an alanine residue, a serine residue and a cysteine residue.

Claim 8 (Original): The method according to Claim 7, wherein the region containing the loop structure existing between β2 and β3 is replaced with an amino acid sequence composed of four glycine residues.

Claim 9 (Currently Amended): The method ~~according to Claim 1~~ for producing a protein having an antithrombotic activity, which comprises replacing, in a protein that has an amino acid sequence of SEQ ID NO: 1 and forms a tertiary structure, from N-terminus to C-terminus, composed of a first β strand (β1), a first a helix (αl), a second α helix (α2), a second β strand (β2), a loop, a third β strand (β3), a fourth β strand (β4) and a fifth β strand (β5) in this order from the amino terminus, at least one amino acid residue in a region from α2 to β2, a region from β3 to β4, or in the regions from α2 to β2 and from β3 to β4 so that electric charge of the amino acid residue is substituted towards positive direction as compared to the unsubstituted amino acid,

which further comprises covalently bonding a polyoxyalkylpolyol group to the protein.

Claim 10 (Previously Presented): The method according to Claim 9, wherein the protein contains a cysteine residue corresponding to a cysteine residue of the amino acid residue 81 in the amino acid sequence of SEQ ID NO: 1, and the polyoxyalkylpolyol group is bonded to said cysteine residue.

Claim 11 (Previously Presented): The method according to Claim 9, wherein the polyoxyalkylpolyol group is a polyethylene glycol group.

Claims 12 - 34 (Canceled)